

Figure 1

ERRL1	MAGNDCGALLDEELSSFFLNLYLSDTQGGDSGEEQ-LCADLPELDLSQLDASDFDSATCLG	59
PGC-1	MAWDMCSQDSVWSIDIECAALVGEDQPLCPDLPELDLSELDVNDLDTDSFLG	51

ERRL1	ELQWCPETSETEPSQYSPDDSELFQ-IDSENEA-LLAALTKTLDDIPEDDVGLAAPPELD	117
PGC-1	GLKWCSQSEIISNQYNNEPANIFEKIDEENEANLLAVLTETLDSLFVDEDEGLPSTFALT	111

ERRL1	EGDTPSCTPASAPPLSAPPSPTLERLLSPASDVDELSELLQKLLLATSSPTASSDALKDGA	177
PGC-1	DGAVTTDNEASPSSM---PDGT-----PPQEAEEFSLKKLLAPANTQLSYNECSGLS	163

ERRL1	TWSQTSLS---RSQRPCVKVDGTQDKKPTL---RAQSRPCTELHKHLTSVLPCPRVK	230
PGC-1	TQNHAAHNHTRIRTNPAIVKTENSWSNKAKSICQQQKPPRRPCSELLKYLTNDPPHTK	223

ERRL1	ACSPTFHPSRLLSKEE-----EEVGEDCPSPW--LTPASQDLSAQDTASPDQAQPF	282
PGC-1	PTENRNSSRDKCAKSKSHTQPSQHAQAKPTTSLPLTPESPNDP---KGSFFEN---	276

ERRL1	EEDVRAMVQLIRYMHTYCLPQRKLPQRAPEPIFOACSSLSRQVQPRSRHPKAFWTEFSI	341
PGC-1	-----	
ERRL1	LRELLAQDILCDVSKPYRLAIPVYASLTPQSRPRPFKDSQASPAHSAMAEVRITASPKS	401
PGC-1	-----	
ERRL1	TGPRPSLRPLRLLEVKRVDUNKPTRQKREDEEEEEEEEEEEEEKEEEEEEWGRKRFGRLP	461
PGC-1	-----	
ERRL1	WTKLGRKMDSSVCPVRRSRRLNPELGPWLTFDEPLGALPSMCLDTETHNLEEDLGSITD	521
PGC-1	-----	
ERRL1	SSQGRQLPQGSQIPALESFCESGCGDTDEDPCFPQPTSRDSSRCLMLALSQSDSLGKXSF	581
PGC-1	-----KTI	279

ERRL1	BESLTVELCGTAGLTPPTTPPYKMEEDPFKPDTKLSPGQDTAPSLPSPEAL--PLTATP	639
PGC-1	ERTLSVELSGTAGLTPPTTPPHKANQDNPFKASPKLPCKTVVFPPTKRARYSECSGTQ	339

ERRL1	GASHKLPRKHPERSEILSHLQHAT--TQPVSQAGQKRPFCSCSFGDHDYQVLRPEAALQR	697
PGC-1	G-SHST-KKGPEQSEIYAQLSKSSGLSRGHEERKTKRPSLRLFGDHDYQVLSNKTDLI	397

ERRL1	KV---LRSWEPGVHLEDLAQQGAPLPTETKAP---RR--EANQCDPTHKDSMQLRDHE	749
PGC-1	NISQELQDSRQLDFKQDASCDWQHICSSDTSQCYLRETLEASKQVSPCSTRK-QLQDQE	456

ERRL1	IRASLTKHFGLETALEGEDLASCKSPEDTVFEDSSSS-----SGES-SFLEEEEE	802
PGC-1	IRAEINXKHFGHPCQAVF-DDKSDKTSELRDGDFSNEQFSKLPVFINSGLAMDGLFDDSED	515

ERRL1	EEEGGEEDDEGEDS---GVSEPCSD-HCFYQ---SPP---SKASRQLCSFRRSSSGSS	851
PGC-1	ESDKLSYPWDGTQPYSLFDVSPSCSSFNSPCRDSVSPPKSLFSQRPQMRSSRSFRRNB	575

ERRL1	SCS-----SWSPATRIQ-----FRRESRGPCS-----DG	875
PGC-1	SCRSRSPYRSRSPGSRSSRSRSCYVYESSHYRHRTHRNSPLYVRSRSPYRRPYDS	635

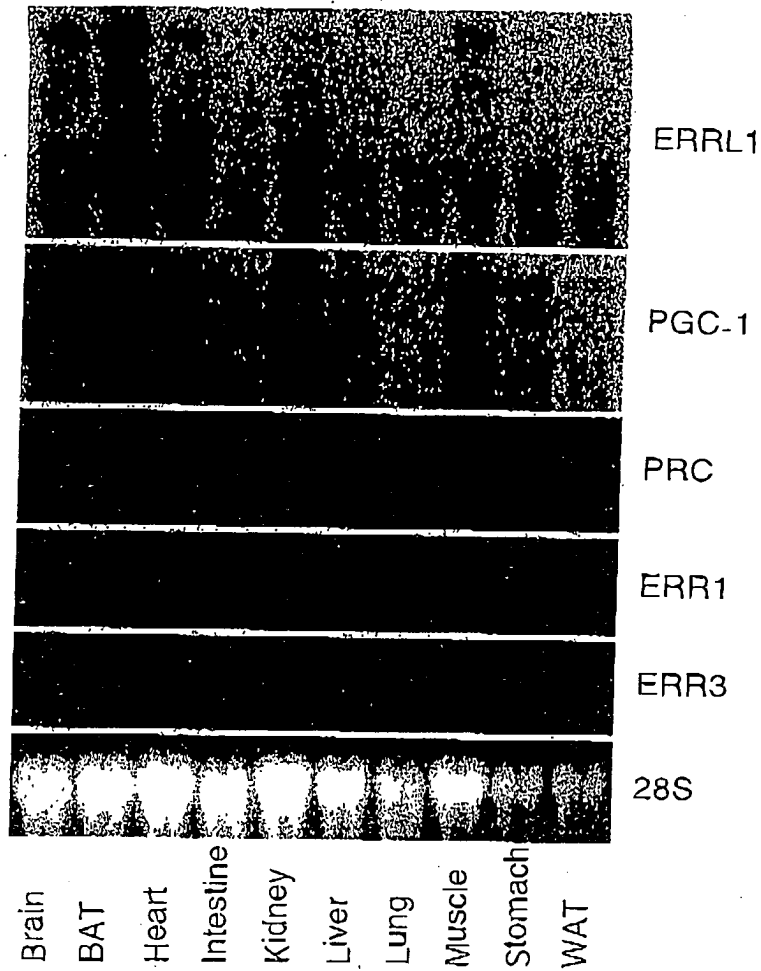
ERRL1	TPSVRHAR-----KRRE-----KAIGEGHVVYIRNLSSDMSSRELKRR	913
PGC-1	YEAYEHERLKRDEYRKEHEKRESERAKORERQKQKAIERHVIYVGKIRPDTTRTELDR	695

ERRL1	FEVFGIVECQVLTIRSKRGQKHGFIATR--CSEHAALSVRNGATLKRNEPSFHLSYGGL	971
PGC-1	FEVFGIEIECTVNIIRDD-GDSYGFITYRYTCDAFAL--ENGYTLRSNETDFELYFCGR	752

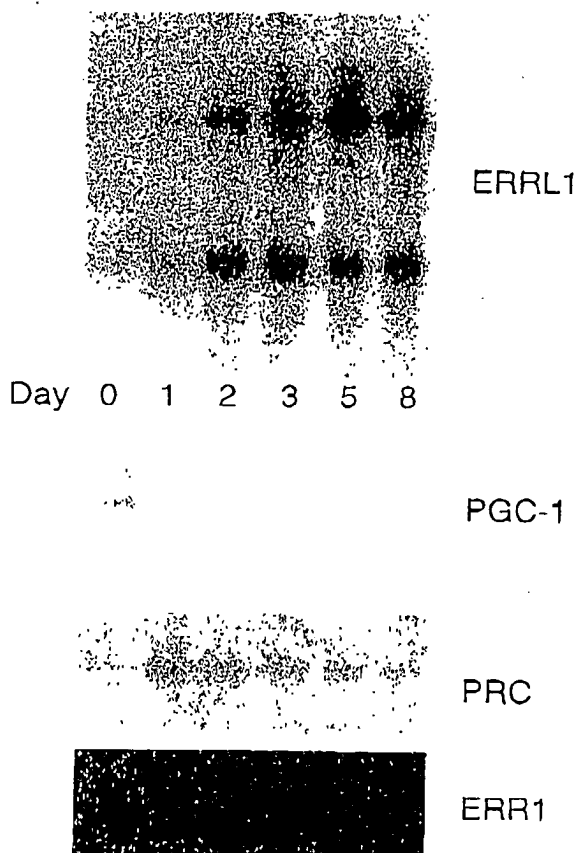
ERRL1	RHFRWPRYTDYDPTSEESLPSSGKSKYEAMDFDSLLKEAQQLH	1014
PGC-1	KQFFKSNYADLDTNSDDFDPASTKSKYDSLDFDSLLKEAQRSLR	796

Figure 2

a



b



c

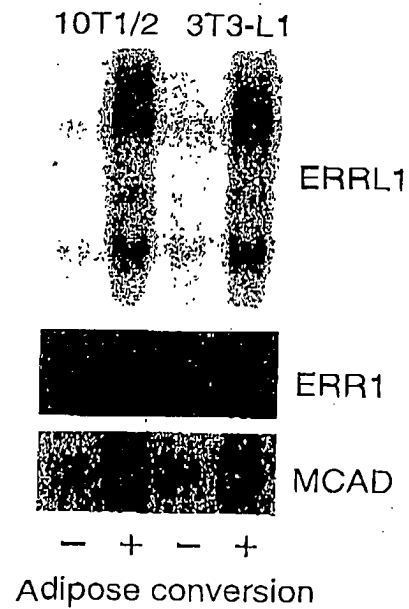


Figure 3

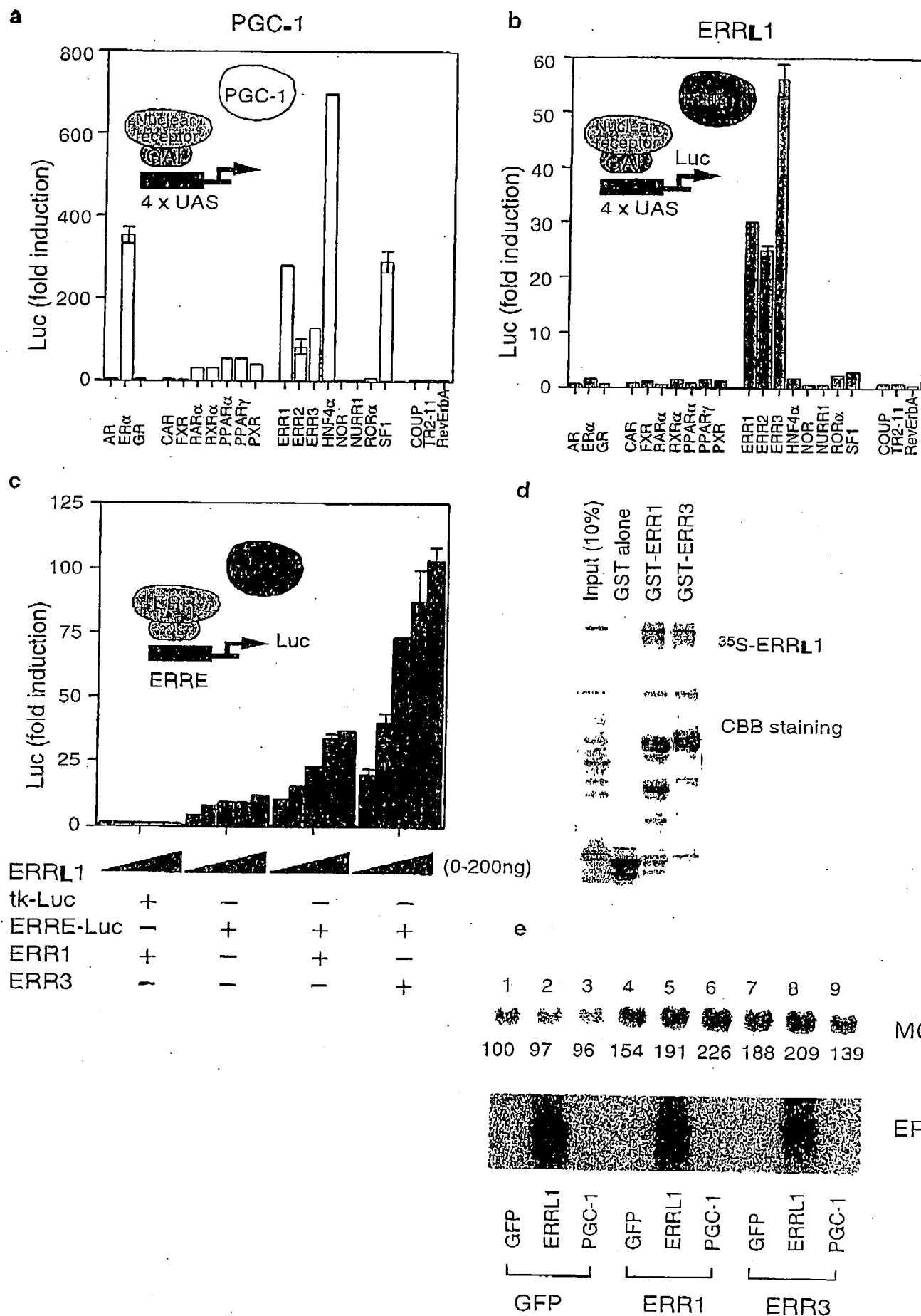


Figure 4

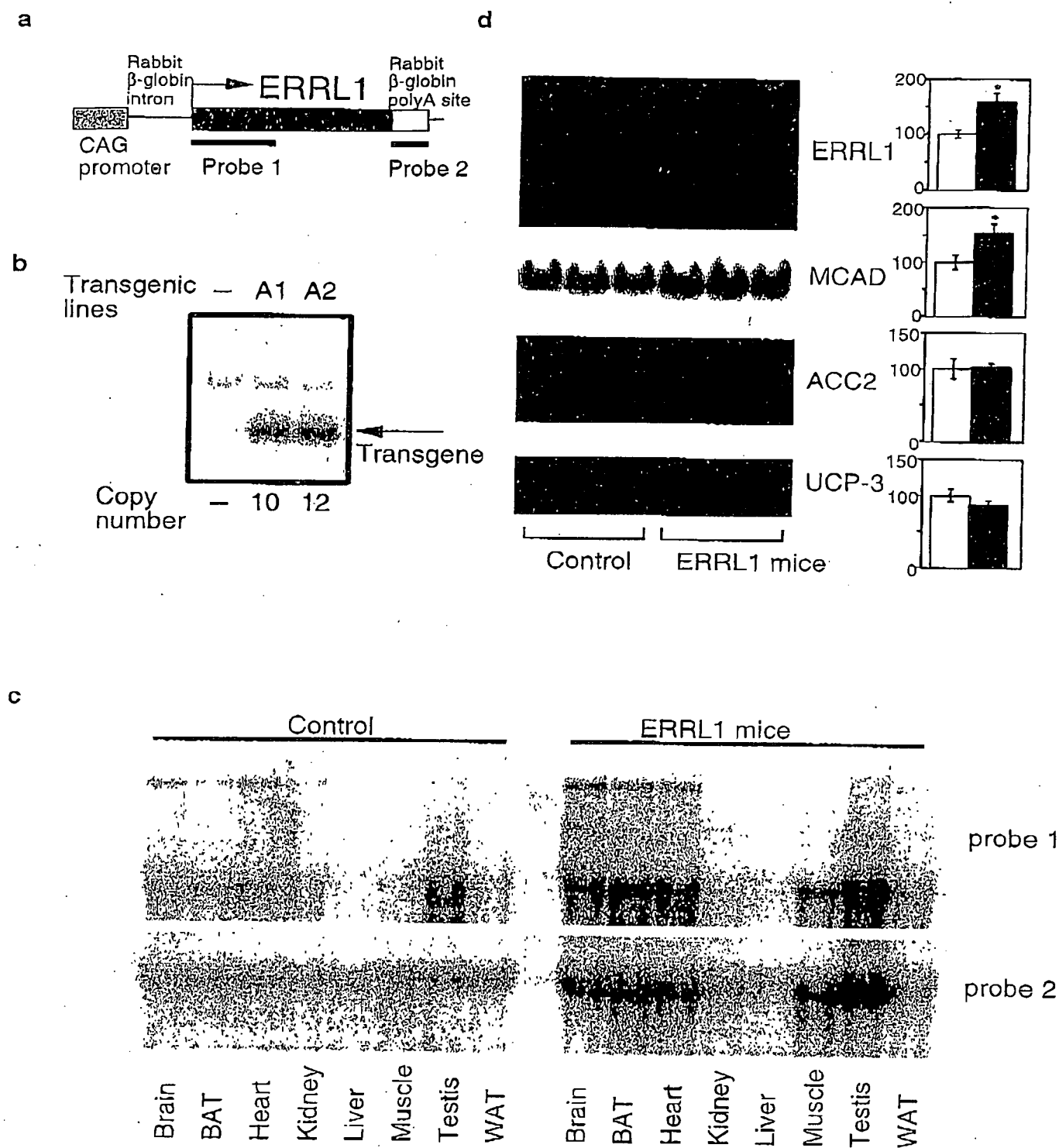


Figure 5

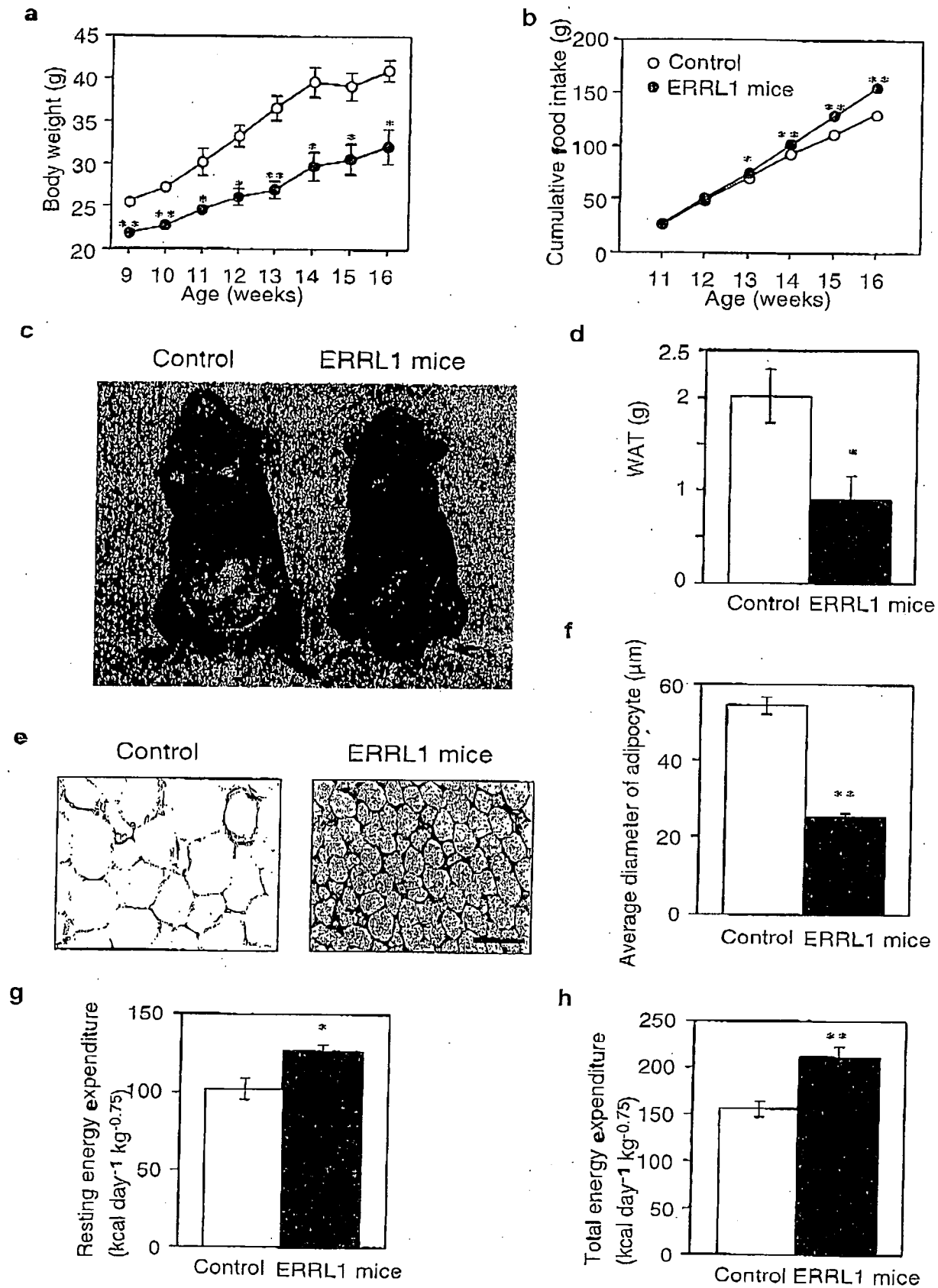


Figure 6

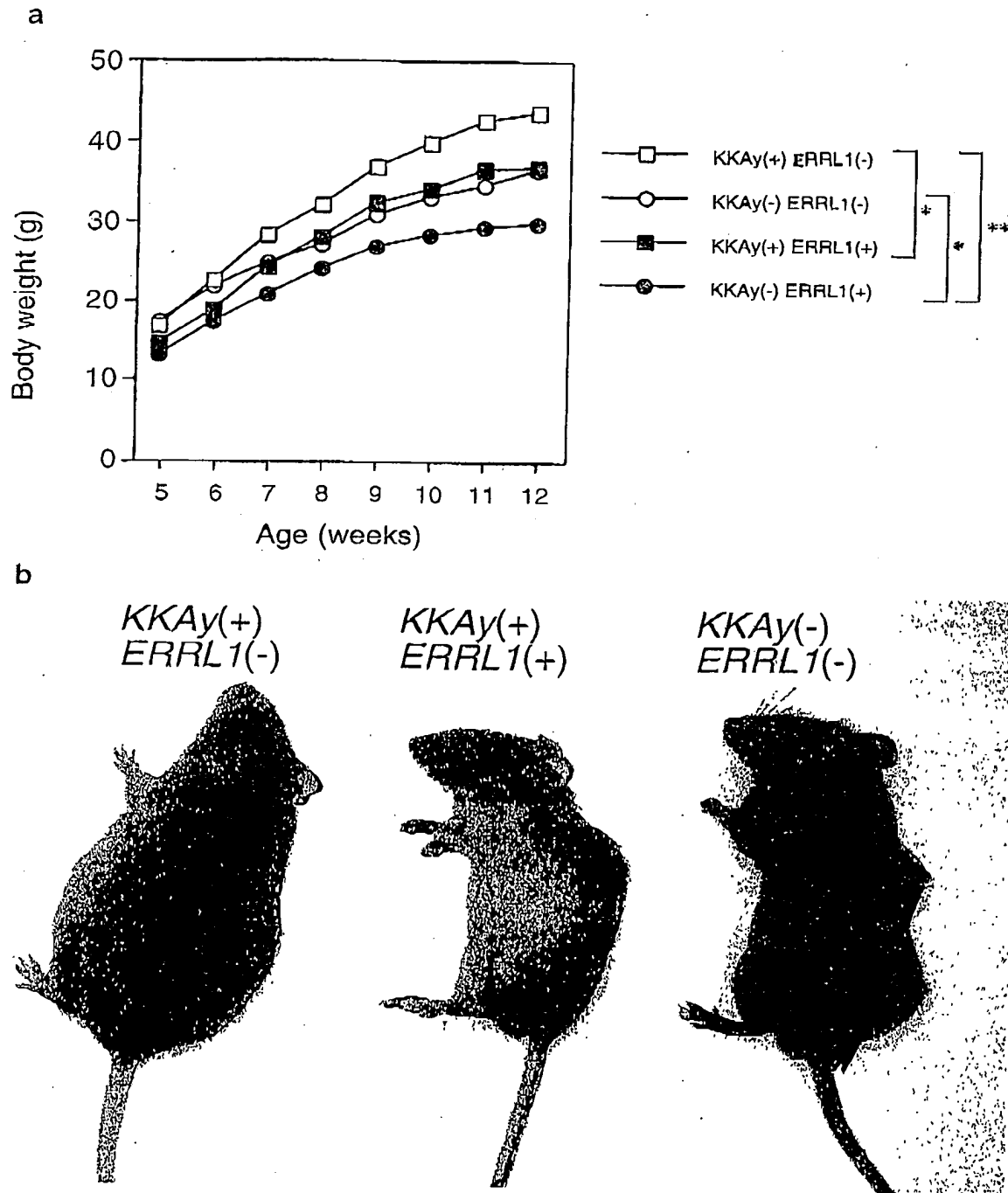
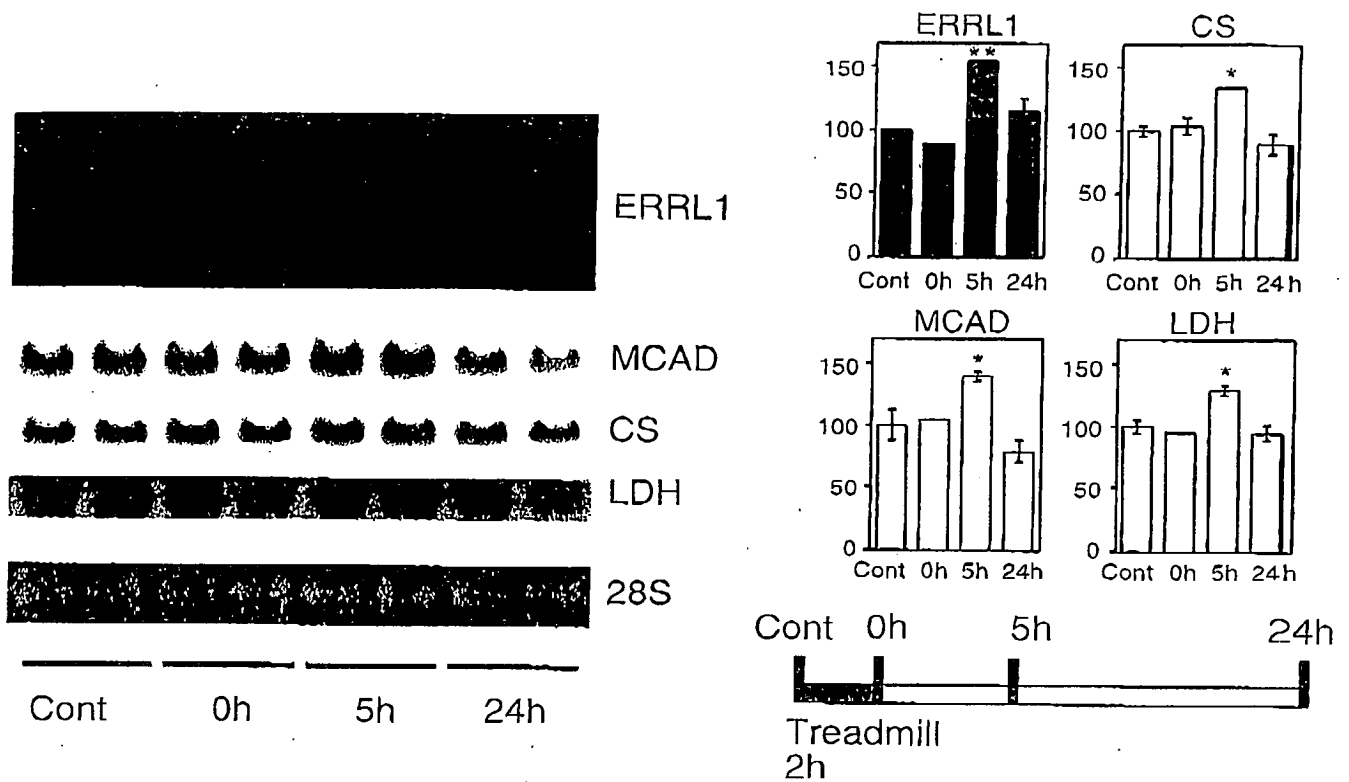


Figure 7

a



b

